

APPENDIX A (Sequence alignment)

RESULT 1

PAK2_HUMAN

ID PAK2_HUMAN STANDARD; PRT; 524 AA.
AC Q13177; Q13154;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 2 (EC 2.7.1.-) (p21-activated
DE kinase 2) (PAK-2) (PAK65) (Gamma-PAK) (S6/H4 kinase).
GN PAK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sells M., Knause U.J., Bagrodia S., Ambrose D., Bokoch G.M.,
RA Chernoff J.;
RL Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 32-524 FROM N.A., AND SEQUENCE OF 401-417.
RC TISSUE=Placenta;
RX MEDLINE=95262637; PubMed=7744004;
RA Martin G.A., Bollag G., McCormick F., Abo A.;
RT "A novel serine kinase activated by rac1/CDC42Hs-dependent
RT autophosphorylation is related to PAK65 and STE20."
RL EMBO J. 14:1970-1978(1995).
RN [3]
RP ERRATUM.
RX MEDLINE=96016211; PubMed=7556080;
RA Martin G.A., Bollag G., McCormick F., Abo A.;
RL EMBO J. 14:4385-4385(1995).
RN [4]
RP AUTOPHOSPHORYLATION.
RX MEDLINE=95403344; PubMed=7673144;
RA Benner G.E., Dennis P.B., Masaracchia R.A.;
RT "Activation of an S6/H4 kinase (PAK 65) from human placenta by
RT intramolecular and intermolecular autophosphorylation."
RL J. Biol. Chem. 270:21121-21128(1995).
CC -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC PHOSPHORYLATES RIBOSOMAL PROTEIN S6, HISTONE H4 AND MYELIN BASIC
CC PROTEIN.
CC -!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1.
CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HIGHER LEVELS SEEN IN
CC SKELETAL MUSCLE, OVARY, THYMUS AND SPLEEN.
CC -!- PTM: Autophosphorylated when activated by CDC42/p21.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC STE20 subfamily.
CC -!- SIMILARITY: Contains 1 CRIB domain.
CC -----
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CC -----
DR EMBL; U24153; AAA65442.1; -.
DR EMBL; U25975; AAA75468.1; -.
DR PIR; S58682; S58682.
DR HSSP; P24941; 1CKP.
DR Genew; HGNC:8591; PAK2.
DR MIM; 605022; -.
DR GO; GO:0004672; F:protein kinase activity; TAS.
DR GO; GO:0006469; P:negative regulation of protein kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000095; PAKbox/Rhobndng.

DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00786; PBD; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS50108; CRIB; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 74 87 CRIB.
 FT DOMAIN 88 248 LINKER.
 FT DOMAIN 249 499 PROTEIN KINASE.
 FT NP_BIND 255 263 ATP (BY SIMILARITY).
 FT BINDING 278 278 ATP (BY SIMILARITY).
 FT ACT_SITE 367 367 BY SIMILARITY.
 FT CONFLICT 90 90 A -> T (IN REF. 2).
 FT CONFLICT 150 150 L -> F (IN REF. 2).
 FT CONFLICT 225 225 P -> T (IN REF. 2).
 FT CONFLICT 329 329 G -> R (IN REF. 2).
 FT CONFLICT 338 338 T -> TA (IN REF. 1).
 SQ SEQUENCE 524 AA; 58004 MW; DB2A7A72BE6B1072 CRC64;

Query Match 100.0%; Score 2707; DB 1; Length 524;
 Best Local Similarity 100.0%; Pred. No. 1.3e-142;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSDNGELEDKPPAPPVRMSSTIFSTGGKDPLSANHSLKPLPSVPPEKKPRHKIISIFSGT	60
Db	1	MSDNGELEDKPPAPPVRMSSTIFSTGGKDPLSANHSLKPLPSVPPEKKPRHKIISIFSGT	60
Qy	61	EKGSKKKEKERPEISPPSDFEHTIHVGFDVAVTGEFTGMPEQWARLLQTSNITKLEQKKNP	120
Db	61	EKGSKKKEKERPEISPPSDFEHTIHVGFDVAVTGEFTGMPEQWARLLQTSNITKLEQKKNP	120
Qy	121	QAVLDVLKFYDSNTVKQKYLSTPPEKDGLPSGTPALNAKGTEAPAVVTEEDDDEETAP	180
Db	121	QAVLDVLKFYDSNTVKQKYLSTPPEKDGLPSGTPALNAKGTEAPAVVTEEDDDEETAP	180
Qy	181	PVIAPRPDHTKSIYTRSVIDPVPAPVGDShVDGAAKSLDKQKKPKMTDEEIMEKLRTIV	240
Db	181	PVIAPRPDHTKSIYTRSVIDPVPAPVGDShVDGAAKSLDKQKKPKMTDEEIMEKLRTIV	240
Qy	241	SIGDPKKKYTRYEKIGQGASGTVFTATDVALGQEVAIKQINLQKQPKKELINEILVMKE	300
Db	241	SIGDPKKKYTRYEKIGQGASGTVFTATDVALGQEVAIKQINLQKQPKKELINEILVMKE	300
Qy	301	LKNPNIVNFLDSYLVGDELFFVMEYLAGGSLTDVVTTETCMDEAQIAAVCRECLQALEFLH	360
Db	301	LKNPNIVNFLDSYLVGDELFFVMEYLAGGSLTDVVTTETCMDEAQIAAVCRECLQALEFLH	360
Qy	361	ANQVIHRDIKSDNVLLGMEGSVKLTDFGFCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAY	420
Db	361	ANQVIHRDIKSDNVLLGMEGSVKLTDFGFCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAY	420
Qy	421	GPKVDIWSLGIMAIEMVEGEPYPYLNENPLRALYLIATNGTPELQNPEKLSPIFRDFLNRC	480
Db	421	GPKVDIWSLGIMAIEMVEGEPYPYLNENPLRALYLIATNGTPELQNPEKLSPIFRDFLNRC	480
Qy	481	LEMDVEKRGSAKELLQHPFLKLAKPLSSLTPLIMAAKEAMKSNR	524
Db	481	LEMDVEKRGSAKELLQHPFLKLAKPLSSLTPLIMAAKEAMKSNR	524